

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Price, Laura A.
Pausch, Mark H.
- (ii) TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
Encoding Them, and Methods of Using Same
- (iii) NUMBER OF SEQUENCES: 56
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: American Home Products Corporation
 - (B) STREET: One Campus Drive
 - (C) CITY: Parsippany
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07054
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 11-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Matthews, Gale F.
 - (B) REGISTRATION NUMBER: 32,269
 - (C) REFERENCE/DOCKET NUMBER: 32,421-C2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-683-2134
 - (B) TELEFAX: 201-683-4117

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 190..2043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGCGATCGC CGCGAGTGTA TATTTTTTTT TTAGCTCAGT CTTCAAGTGTT TCGCGATTCT	60
CTTTAAAGA AAAAAAAAAAT AATAAGTCAA AACTACAAAC CACACAGCGA AAGGCGAAAG	120
CAACGGTTCC TGCGAGTGTT TATTTTTTTT TTCAACAATT TTTGATCGTA GTGCGACAAT	180
CCGTCGAGC ATG TCG CCG AAT CGA TGG ATC CTG CTG CTC ATC TTC TAC	228
Met Ser Pro Asn Arg Trp Ile Leu Leu Ile Phe Tyr	
1 5 10	

ATA TCC TAC CTG ATG TTC GGG GCG GCA ATC TAT TAC CAT ATT GAG CAC	276
Ile Ser Tyr Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His	
15 20 25	
GGC GAG GAG AAG ATA TCG CGC GCC GAA CAG CGC AAG GCG CAA ATT GCA	324
Gly Glu Glu Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala	
30 35 40 45	
ATC AAC GAA TAT CTG CTG GAG GAG CTG GGC GAC AAG AAT ACG ACC ACA	372
Ile Asn Glu Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr	
50 55 60	
CAG GAT GAG ATT CTT CAA CGG ATC TCG GAT TAC TGT GAC AAA CCG GTT	420
Gln Asp Glu Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val	
65 70 75	
ACA TTG CCG CCG ACA TAT GAT GAT ACG CCC TAC ACG TGG ACC TTC TAC	468
Thr Leu Pro Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr	
80 85 90	
CAT GCC TTC TTC TTC GCC TTC ACC GTT TGC TCC ACG GTG GGA TAT GGG	516
His Ala Phe Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly	
95 100 105	
AAT ATA TCG CCA ACC ACC TTC GCC GGA CGG ATG ATC ATG ATC GCG TAT	564
Asn Ile Ser Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr	
110 115 120 125	
TCG GTG ATT GGC ATC CCC GTC AAT GGT ATC CTC TTT GCC GGC CTC GGC	612
Ser Val Ile Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly	
130 135 140	
GAA TAC TTT GGA CGT ACG TTT GAA GCG ATC TAC AGA CGC TAC AAA AAG	660
Glu Tyr Phe Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys	
145 150 155	
TAC AAG ATG TCC ACG GAT ATG CAC TAT GTC CCG CCG CAG CTG GGA TTG	708
Tyr Lys Met Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu	
160 165 170	
ATC ACC ACG GTG GTG ATT GCC CTG ATT CCG GGA ATA GCT CTC TTC CTG	756
Ile Thr Thr Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu	
175 180 185	
GTG CTG CCC TGC GTG GGT GTT CAC CTA CTT CGA GAA CTG GGC CTA TCT	804
Val Leu Pro Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser	
190 195 200 205	
TCC ATC TCG CTG TAC TAC AGC TAT GTG ACC ACC ACA ACA ATT GGA TTC	852
Ser Ile Ser Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe	
210 215 220	
GGT GAC TAT GTG CCC ACA TTT GGA GCC AAC CAG CCC AAG GAG TTC GGC	900
Gly Asp Tyr Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly	
225 230 235	
GGC TGG TTC GTG GTC TAT CAG ATC TTT GTG ATC GTG TGG TTC ATC TTC	948
Gly Trp Phe Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe	
240 245 250	
TCG CTG GGA TAT CTT GTG ATG ATC ATG ACA TTT ATC ACT CGG GGC CTC	996
Ser Leu Gly Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu	
255 260 265	
CAG AGC AAG AAG CTG GCA TAC CTG GAG CAG CAG TTG TCC TCC AAC CTG	1044
Gln Ser Lys Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu	
270 275 280 285	
AAG GCC ACA CAG AAT CGC ATC TGG TCT GGC GTC ACC AAG GAT GTG GGC	1092

Lys	Ala	Thr	Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly		
				290					295					300			
TAC	CTC	CGG	CGA	ATG	CTC	AAC	GAG	CTG	TAC	ATC	CTC	AAA	GTG	AAG	CCT	1140	
Tyr	Leu	Arg	Arg	Met	Leu	Asn	Glu	Leu	Tyr	Ile	Leu	Lys	Val	Lys	Pro		
			305					310					315				
GTG	TAC	ACC	GAT	GTA	GAT	ATC	GCC	TAC	ACA	CTG	CCA	CGT	TCC	AAT	TCG	1188	
Val	Tyr	Thr	Asp	Val	Asp	Ile	Ala	Tyr	Thr	Leu	Pro	Arg	Ser	Asn	Ser		
			320				325					330					
TGT	CCG	GAT	CTG	AGC	ATG	TAC	CGC	GTG	GAG	CCG	GCT	CCC	ATT	CCC	AGC	1236	
Cys	Pro	Asp	Leu	Ser	Met	Tyr	Arg	Val	Glu	Pro	Ala	Pro	Ile	Pro	Ser		
			335			340					345						
CGG	AAG	AGG	GCA	TTC	TCC	GTG	TGC	GCC	GAC	ATG	GTT	GGC	GCC	CAA	AGG	1284	
Arg	Lys	Arg	Ala	Phe	Ser	Val	Cys	Ala	Asp	Met	Val	Gly	Ala	Gln	Arg		
					355					360					365		
GAG	GCG	GGC	ATG	GTA	CAC	GCC	AAT	TCC	GAT	ACG	GAT	CTA	ACC	AAA	CTG	1332	
Glu	Ala	Gly	Met	Val	His	Ala	Asn	Ser	Asp	Thr	Asp	Leu	Thr	Lys	Leu		
				370					375					380			
GAT	CGC	GAG	AAG	ACA	TTC	GAG	ACG	GCG	GAG	GCG	TAC	CAC	CAG	ACC	ACC	1380	
Asp	Arg	Glu	Lys	Thr	Phe	Glu	Thr	Ala	Glu	Ala	Tyr	His	Gln	Thr	Thr		
			385					390					395				
GAT	TTG	CTG	GCC	AAG	GTG	GTC	AAC	GCA	CTG	GCC	ACG	GTG	AAG	CCA	CCG	1428	
Asp	Leu	Leu	Ala	Lys	Val	Val	Asn	Ala	Leu	Ala	Thr	Val	Lys	Pro	Pro		
			400				405					410					
CCG	GCG	GAA	CAG	GAA	GAT	GCG	GCT	CTC	TAT	GGT	GGC	TAT	CAT	GGC	TTC	1476	
Pro	Ala	Glu	Gln	Glu	Asp	Ala	Ala	Leu	Tyr	Gly	Gly	Tyr	His	Gly	Phe		
			415			420					425						
TCC	GAC	TCC	CAG	ATC	CTG	GCC	AGC	GAA	TGG	TCG	TTC	TCG	ACG	GTC	AAC	1524	
Ser	Asp	Ser	Gln	Ile	Leu	Ala	Ser	Glu	Trp	Ser	Phe	Ser	Thr	Val	Asn		
					435					440					445		
GAG	TTC	ACA	TCA	CCG	CGA	CGT	CCA	AGA	GCA	CGT	GCC	TGC	TCC	GAT	TTC	1572	
Glu	Phe	Thr	Ser	Pro	Arg	Arg	Pro	Arg	Ala	Arg	Ala	Cys	Ser	Asp	Phe		
				450					455					460			
AAT	CTG	GAG	GCA	CCT	CGC	TGG	CAG	AGC	GAG	AGG	CCA	CTG	CGT	TCG	AGC	1620	
Asn	Leu	Glu	Ala	Pro	Arg	Trp	Gln	Ser	Glu	Arg	Pro	Leu	Arg	Ser	Ser		
			465					470					475				
CAC	AAC	GAA	TGG	ACA	TGG	AGC	GGC	GAC	AAC	CAG	CAG	ATC	CAG	GAG	GCA	1668	
His	Asn	Glu	Trp	Thr	Trp	Ser	Gly	Asp	Asn	Gln	Gln	Ile	Gln	Glu	Ala		
			480				485					490					
TTC	AAC	CAG	CGC	TAC	AAG	GGA	CAG	CAG	CGT	GCC	AAC	GGA	GCA	GCC	AAC	1716	
Phe	Asn	Gln	Arg	Tyr	Lys	Gly	Gln	Gln	Arg	Ala	Asn	Gly	Ala	Ala	Asn		
			495			500					505						
TCG	ACC	ATG	GTC	CAT	CTG	GAG	CCG	GAT	GCT	TTG	GAG	GAG	CAG	CTG	AGA	1764	
Ser	Thr	Met	Val	His	Leu	Glu	Pro	Asp	Ala	Leu	Glu	Glu	Gln	Leu	Arg		
					515					520					525		
AAC	AAT	CAC	CGG	GTG	CCG	GTC	GCG	TCA	AGA	AGT	TCT	CCA	TGC	CGG	ATG	1812	
Asn	Asn	His	Arg	Val	Pro	Val	Ala	Ser	Arg	Ser	Ser	Pro	Cys	Arg	Met		
				530					535					540			
GTC	TGC	GAC	GTC	TGT	TTC	CCT	TCC	AGA	AGA	AGC	ACC	CCT	CGC	AGG	ATC	1860	
Val	Cys	Asp	Val	Cys	Phe	Pro	Ser	Arg	Arg	Ser	Thr	Pro	Arg	Arg	Ile		
			545					550					555				
TGG	AGC	GCA	AGT	TGT	CCG	TGG	TCT	CGG	TAC	CCG	AGG	GTG	TCA	TCT	CGC	1908	
Trp	Ser	Ala	Ser	Cys	Pro	Trp	Ser	Arg	Tyr	Pro	Arg	Val	Ser	Ser	Arg		

00016011.031197

560	565	570	
AGG AAG CCA GAT CCC CGC TGG ACT ACT ACA TCA ACA CGG TCA CGG CGG			1956
Arg Lys Pro Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg			
575	580	585	
CCT CCA GTC AAT CCT ATT TGC GCA ACG GAC GCG GTC CGC CAC CGC CCT			2004
Pro Pro Val Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro			
590	595	600	605
TCG AAT CGA ATG GCA GCT TGG CCA GCG GCG GCG GCG GGC TAACGAACAT			2053
Ser Asn Arg Met Ala Ala Trp Pro Ala Ala Ala Gly			
610	615		
GGGCTTCCAG ATGGAGGATG GAGCAACCCC GCCATCGGCA TTGGGCGGTG GAGCCTATCA			2113
ACGCAAGGCG GCTGCTGGCA AGCGCCGACG CGAGAGCATC TACACCCAGA ATCAAGCCCC			2173
ATCCGCTCGC CGGGGCAGCA TGTATCCGCC GACCGCGCAC GCCTTGGCCC AGATGCAGAT			2233
GCGACGCGGC AGCTTGGCAA CCAGTGGCTC TGGATCGGCG GCCATGGCGG CAGTGGCCGC			2293
GCGTCGTGGC AGCCTCTTCC CAGCTACAGC ATCGGCATCA TCGCTGACCT CTGCTCCGCG			2353
CCGAAGCAGC ATATTCTCGG TTACCTCCGA AAAGGATATG AATGTGCTGG AGCAGACGAC			2413
CATTGCGGAT CTGATTCTGTG CGCTCGAG			2441

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Pro	Asn	Arg	Trp	Ile	Leu	Leu	Leu	Ile	Phe	Tyr	Ile	Ser	Tyr
1				5					10					15	
Leu	Met	Phe	Gly	Ala	Ala	Ile	Tyr	Tyr	His	Ile	Glu	His	Gly	Glu	Glu
			20					25					30		
Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	Ile	Asn	Glu
		35					40					45			
Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu
	50					55					60				
Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro
65					70				75					80	
Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
			85					90						95	
Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser
		100						105					110		
Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile
	115					120					125				
Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe
	130					135					140				
Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met
145					150					155					160

Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
530 535 540

Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
545 550 555 560

Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
565 570 575

Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
580 585 590

Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
595 600 605

Met Ala Ala Trp Pro Ala Ala Ala Ala Gly
610 615

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG TCC GAT CAG CTG TTT GTC GCA TTT GAG AAG TAT TTC TTG ACG AGT	48
Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser	
1 5 10 15	
AAC GAG GTC AAG AAG AAT GCA GCA ACG GAG ACA TGG ACA TTT TCA TCG	96
Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser	
20 25 30	
TCC ATT TTC TTT GCC GTA ACC GTC GTC ACT ACC ATC GGA TAC GGT AAT	144
Ser Ile Phe Phe Ala Val Thr Val Thr Thr Ile Gly Tyr Gly Asn	
35 40 45	
CCA GTT CCA GTG ACA AAC ATT GGA CGG ATA TGG TGT ATA TTG TTC TCC	192
Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser	
50 55 60	
TTG CTT GGA ATA CCT CTA ACA CTG GTT ACC ATC GCT GAC TTG GCA GGT	240
Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly	
65 70 75 80	
AAA TTC CTA TCT GAA CAT CTT GTT TGG TTG TAT GGA AAC TAT TTG AAA	288
Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys	
85 90 95	
TTA AAA TAT CTC ATA TTG TCA CGA CAT CGA AAA GAA CGG AGA GAG CAC	336
Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His	
100 105 110	
GTT TGT GAG CAC TGT CAC AGT CAT GGA ATG GGG CAT GAT ATG AAT ATC	384
Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile	
115 120 125	
GAG GAG AAA AGA ATT CCT GCA TTC CTG GTA TTA GCT ATT CTG ATA GTA	432
Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val	

130	135	140	
TAT ACA GCG TTT GGC GGT GTC CTA ATG TCA AAA TTA GAG CCG TGG TCT			480
Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser			
145	150	155	160
TTC TTC ACT TCA TTC TAC TGG TCC TTC ATT ACA ATG ACT ACT GTC GGG			528
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly			
	165	170	175
TTT GGC GAC TTG ATG CCC AGA AGG GAC GGA TAC ATG TAT ATC ATA TTG			576
Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu			
	180	185	190
CTC TAT ATC ATT TTA GGT AAA TTT TCA ATG AAA AAA AAA CAA AAA TTC			624
Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe			
	195	200	205
AAA ATA TTT TTA GGT CTT GCA ATA ACT ACA ATG TGC ATT GAT TTG GTA			672
Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val			
	210	215	220
GGA GTA CAG TAT ATT CGA AAG ATT CAT TAT TTC GGA AGA AAA ATT CAA			720
Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln			
	225	230	235
GAC GCT AGA TCT GCA TTG GCG GTT GTA GGA GGA AAG GTA GTC CTT GTA			768
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val			
	245	250	255
TCA GAA CTC TAC GCA AAT TTA ATG CAA AAG CGA GCT CGT AAC ATG TCC			816
Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser			
	260	265	270
CGA GAA GCT TTT ATA GTG GAG AAT CTC TAT GTT TCC AAA CAC ATC ATA			864
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile			
	275	280	285
CCA TTC ATA CCA ACT GAT ATC CGA TGT ATT CGA TAT ATT GAT CAA ACT			912
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr			
	290	295	300
GCC GAT GCT GCT ACC ATT TCC ACG TCA TCG TCT GCA ATT GAT ATG CAA			960
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln			
	305	310	315
AGT TGT AGA TTT TGT CAT TCA AGA TAT TCT CTC AAT CGT GCA TTC AAA			1008
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys			
	325	330	335
TAG			1011

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Asp	Gln	Leu	Phe	Val	Ala	Phe	Glu	Lys	Tyr	Phe	Leu	Thr	Ser
1				5					10					15	
Asn	Glu	Val	Lys	Lys	Asn	Ala	Ala	Thr	Glu	Thr	Trp	Thr	Phe	Ser	Ser
		20						25					30		

000001070

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCATTTTCT TTGCCGTAAC CGTCGTCACCT ACCATCGGAT ACGGTAATCC A

51

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCATTCTACT GGTCTTCAT TACAATGACT ACTGTCGGGT TTGGCGACTT G

51

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
1 5 10 15

Arg Cys Val Thr Asp Glu Cys Pro
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
1 5 10 15

Arg Cys Val Thr Glu Gln Cys Ala
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20250110 1419

Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr
 1 5 10 15
 Arg Tyr Ile Thr Asp His Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn
 1 5 10 15
 Ile Ser Pro Thr Thr Phe Ala Gly
 20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly Asp
 1 5 10 15
 Met Thr Pro Val Gly Phe Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly Tyr Gly Asp
 1 5 10 15
 Met Val Pro Glu Thr Ile Ala Gly
 20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

03916011.031197

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly Tyr Gly Asp
1 5 10 15
Ile Cys Pro Thr Thr Ala Leu Gly
20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly Tyr Gly Asp
1 5 10 15
Met Ala Pro Lys Thr Tyr Ile Gly
20

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly Phe Gly Asn
1 5 10 15
Val Ala Ala Glu Thr Asp Asn Glu
20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly Tyr Gly Asp
1 5 10 15
Val Tyr Cys Glu Thr Val Leu Gly
20

08616041.0349

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser Leu Tyr Thr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp
1 5 10 15

Tyr Val Pro Thr Phe Gly Ala Asn
 20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Phe Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn
1 5 10 15

Ile Ser Pro Thr Thr Phe Ala Gly
 20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
1 5 10 15

Pro Val Pro Val Thr Asn Thr Gly
 20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

0001501.03149

Ser Leu Tyr Thr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp
 1 5 10 15
 Tyr Val Pro Thr Phe Gly Ala Asn
 20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly Phe Gly Asp
 1 5 10 15
 Leu Met Pro Arg Arg Asp Gly Tyr
 20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATAAAGCTTA AAAATGTCGC CGAATCGATG GAT

33

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCTCTAGAC CTCCATCTGG AAGCCCATGT

30

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAAAGCTTA AAATGGCACA CATCACG

27

00016011.031197

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAACTCGAGT CATACCTGTG GACT

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAAAAGCTTA AAATGGTCGG GCAATTG

27

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAAAGCATGC TCATCTGGAT GGGCA

25

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAAAAGCTTA AAATGGCCTC GGTCGCC

27

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

00015011.031197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTCTAGAC TACATCGTTG TCTT

24

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAAGCTTA AAATGAATCT GATCAAC

27

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAATCTAGAT TAGTCGAAAC TGAA

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAAAAGCTTA AAATGCCTGG CGGA

24

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAATCTAGAG GCTACAGGAA GTCC

24

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs

0001601 0349

0000103197

GGGGGTACCA AAATGTCGGG GTGTGAT

-27-

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

TTTTTCTAGA TCAAGAGTTA TCATC

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

ATGGTAATAA	TCAACCGATC	GAACACCTAT	GCCGTTGAGC	AGGAAGCATT	TCCAAGAGAC	60
AAGTACAATA	TTGTCTACTG	GCTCGTCATT	CTTGTTGGAT	TCGGAGTTCT	TCTGCCATGG	120
AATATGTTCA	TTACTATCGC	CCCTGAGTAT	TATGTGAATT	ATTGGTTCAA	ACCGGATGGC	180
GTGGAGACAT	GGTATTCGAA	AGAATTCATG	GGATCTTTGA	CGATTGGCTC	ACAAC'TTCCA	240
AACGCAAGCA	TTAATGTTTT	CAACCTGTTT	CTCATTATTG	CTGGTCCCCT	GATCTACCGC	300
GTCTTTGCTC	CGGTTTGCTT	CAACATCGTC	AACCTGACAA	TCATTCTCAT	CCTCGTCATT	360
GTTCTGGAGC	CCACTGAAGA	TTCCATGTCC	TGGTTTTTCT	GGGTAAC'TCT	TGGAATGGCG	420
ACTTCAATCA	ATTTTAGCAA	TGGGCTATAT	GAAAACTCGG	TTTATGGAGT	TGGTGGCGAT	480
TTTCCGCACA	CCTACATTGG	CGCTCTCTTG	ATTGGAAACA	ACATTTGCGG	ATTGCTGATA	540
ACG GTTGTGA	AAATCGGAGT	GACCTATTTT	CTGAATGATG	AGCCTAAACT	TGTTGCAATC	600
GTCTATTTTCG	GCATATCGTT	GGTGATCCTT	CTGGTGTGTG	CAATTGCACT	TTTCTTTATC	660
ACAAAGCAAG	ATTTCTACCA	CTATCACCAT	CAAAAAGGAA	TGGAAATTCG	CGAAAAGGCG	720
GAAACCGACA	GACCGTCTCC	ATCCATTCTT	TGGACCACAT	TCACAAACTG	TTATGGGCAA	780
CTCTTCAATG	TTTG GTTCTG	CTTTGCCGTT	ACTCTCACAA	TCTTCCCTGT	TATGATGACC	840
GTTACCACTC	GTGGAGATTG	CGGCTTCCTA	AACAAAATTA	TGTCTGAAAA	CGATGAAATC	900

TACACTTTGC TCACAAGTTT CCTCGTCTTC AATTTGTTCG CTGCGATTGG ATCCATAGTT 960
 GCTTCCAAGA TTCACTGGCC GACACCCCGT TACCTCAAAT TTGCCATAAT CTTGCGTGCT 1020
 CTTTTCATTC CATTCTTCTT CTTCTGCAAC TATCGTGTCC AGACGCGTGC TTATCCTGTT 1080
 TTCTTTGAGT CTA CTGACAT TTTTGTGATT GGTGGAATTG CCATGTCTTT TTCACATGGA 1140
 TACCTCAGCG CTCTGGCAAT GGGATACACT CCAAACGTCG TGCCATCTCA CTACTCAAGA 1200
 TTTGCCGCTC AGCTTTCCGT TTGCACTCTT ATGGTTGGCC TTCTCACCGG TGGCCTGTGG 1260
 CCCGTTGTTA TTGAGCACTT CGTGACAAG CCAAGTATCT TATAAATATT TATAGCATTA 1320
 GAGTATACTT GTTATATGTT GTTTTATTA AGCTGTGGAA TAAATAATT ATTA AAAAAA 1380
 AAAAAAAAAA AAAA 1394

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 479 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ser	Pro	Asn	Arg	Trp	Ile	Leu	Leu	Leu	Ile	Phe	Tyr	Ile	Ser	Tyr
1				5					10					15	
Leu	Met	Phe	Gly	Ala	Ala	Ile	Tyr	Tyr	His	Ile	Glu	His	Gly	Glu	Glu
			20					25					30		
Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	Ile	Asn	Glu
		35					40					45			
Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu
	50					55					60				
Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro
65					70					75				80	
Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
				85					90					95	
Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser
			100					105					110		
Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile
			115				120					125			
Gly	Ile	Pro	Val	Asn	Gly	Ile	Leu	Phe	Ala	Gly	Leu	Gly	Glu	Tyr	Phe
	130					135					140				
Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	Tyr	Lys	Met
145					150					155					160
Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	Ile	Thr	Thr
				165					170					175	
Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro
			180					185					190		
Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser

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	195					200					205				
Leu	Tyr 210	Tyr	Ser	Tyr	Val	Thr 215	Ile	Thr	Thr	Ile	Gly 220	Phe	Gly	Asp	Tyr
Val 225	Pro	Thr	Phe	Gly	Ala 230	Asn	Gln	Pro	Lys	Glu 235	Phe	Gly	Gly	Trp	Phe 240
Val	Val	Tyr	Gln	Ile 245	Phe	Val	Ile	Val	Trp 250	Phe	Ile	Phe	Ser	Leu 255	Gly
Tyr	Leu	Val	Met 260	Ile	Met	Thr	Phe	Ile 265	Thr	Arg	Gly	Leu	Gln 270	Ser	Lys
Lys	Leu	Ala 275	Tyr	Leu	Glu	Gln	Gln 280	Leu	Ser	Ser	Asn	Leu 285	Lys	Ala	Thr
Gln	Asn 290	Arg	Ile	Trp	Ser	Gly 295	Val	Thr	Lys	Asp	Val 300	Gly	Tyr	Leu	Arg
Arg 305	Met	Leu	Asn	Glu	Leu 310	Tyr	Ile	Leu	Lys	Val 315	Lys	Pro	Val	Tyr	Thr 320
Asp	Val	Asp	Ile	Ala 325	Tyr	Thr	Leu	Pro	Arg 330	Ser	Asn	Ser	Pro	Leu 335	Ser
Met	Tyr	Arg	Val 340	Glu	Pro	Ala	Pro	Ile 345	Pro	Ser	Arg	Lys	Arg 350	Ala	Phe
Ser	Val	Cys 355	Ala	Asp	Met	Val	Gly 360	Ala	Gln	Arg	Glu	Ala 365	Gly	Met	Val
His 370	Ala	Asn	Ser	Asp	Thr	Asp 375	Leu	Thr	Lys	Leu	Asp 380	Arg	Glu	Lys	Thr
Phe 385	Glu	Thr	Ala	Glu	Ala 390	Tyr	His	Gln	Thr	Thr 395	Asp	Leu	Leu	Ala	Lys 400
Val	Val	Asn	Ala	Leu 405	Ala	Thr	Val	Lys	Pro 410	Pro	Pro	Ala	Leu	Gln 415	Glu
Asp	Ala	Ala	Leu 420	Tyr	Gly	Gly	Tyr	His 425	Gly	Phe	Ser	Asp	Ser 430	Gln	Ile
Leu	Ala	Ser 435	Glu	Trp	Ser	Phe	Ser 440	Thr	Val	Asn	Glu	Phe 445	Thr	Ser	Pro
Arg	Arg 450	Pro	Arg	Ala	Arg	Ala 455	Cys	Ser	Asp	Phe	Asn 460	Leu	Glu	Ala	Pro
Arg 465	Trp	Gln	Ser	Glu	Arg 470	Pro	Leu	Arg	Ser	Ser 475	His	Asn	Glu	Trp	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
1 5 10 15

Asn	Glu	Val	Lys 20	Lys	Asn	Ala	Ala	Thr 25	Glu	Thr	Trp	Thr	Phe 30	Ser	Ser
Ser	Ile	Phe 35	Phe	Ala	Val	Thr	Val 40	Val	Thr	Thr	Ile	Gly 45	Tyr	Gly	Asn
Pro	Val 50	Pro	Val	Thr	Asn	Ile 55	Gly	Arg	Ile	Trp	Ile 60	Leu	Phe	Ser	Leu
Ile 65	Gly	Ile	Pro	Leu	Thr 70	Leu	Val	Thr	Ile	Ala 75	Leu	Ala	Gly	Lys	Phe 80
Leu	Ser	Glu	His 85	Leu	Val	Trp	Leu	Tyr	Gly 90	Asn	Tyr	Leu	Lys	Leu 95	Lys
Tyr	Leu	Ile	Leu 100	Ser	Arg	His	Arg	Lys 105	Glu	Arg	Arg	Glu	His 110	Val	Cys
Glu	His	Cys 115	His	Ser	His	Gly	Met 120	Gly	His	Asp	Met	Asn 125	Ile	Glu	Glu
Lys	Arg 130	Ile	Pro	Ala	Phe	Leu 135	Val	Leu	Ala	Ile	Leu 140	Ile	Val	Tyr	Thr
Ala 145	Phe	Gly	Gly	Val	Leu 150	Met	Ser	Lys	Leu	Glu 155	Pro	Trp	Ser	Phe	Phe 160
Thr	Ser	Phe	Tyr 165	Trp	Ser	Phe	Ile	Thr	Met 170	Thr	Thr	Val	Gly	Phe 175	Gly
Asp	Leu	Met	Pro 180	Arg	Arg	Asp	Gly	Tyr 185	Met	Tyr	Ile	Ile	Leu 190	Leu	Tyr
Ile	Ile	Leu 195	Gly	Lys	Phe	Ser	Met 200	Lys	Lys	Lys	Gln	Lys 205	Phe	Lys	Ile
Phe 210	Leu	Gly	Leu	Ala	Ile	Thr 215	Thr	Met	Cys	Ile	Asp 220	Leu	Val	Gly	Val
Gln 225	Tyr	Ile	Arg	Lys	Ile 230	His	Tyr	Phe	Gly	Arg 235	Lys	Ile	Gln	Asp	Ala 240
Arg	Ser	Ala	Leu	Ala 245	Val	Val	Gly	Gly	Lys 250	Val	Val	Leu	Val	Ser 255	Glu
Leu	Tyr	Ala	Asn 260	Leu	Met	Gln	Lys	Arg 265	Ala	Arg	Asn	Met	Ser 270	Arg	Glu
Ala	Phe 275	Ile	Val	Glu	Asn	Leu	Tyr 280	Val	Ser	Lys	His 285	Ile	Ile	Pro	Phe
Ile	Pro 290	Thr	Asp	Ile	Arg	Cys 295	Ile	Arg	Tyr	Ile	Asp 300	Gln	Thr	Ala	Asp
Ala 305	Ala	Thr	Ile	Ser	Thr 310	Ser	Ser	Ser	Ala	Ile 315	Asp	Met	Gln	Ser	Cys 320
Arg	Phe	Cys	His 325	Ser	Arg	Tyr	Ser	Leu	Asn 330	Arg	Ala	Phe	Lys	Xaa 335	

(2) INFORMATION FOR SEQ ID NO:39:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TNGGATATCT GGATGACTAT T

21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGTCATCCAG ATAACTCCAG TACTAGTGT

29

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGCAGGCAGA GCCACAAAGA GTACACAG

28

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGAGATCAGC TAGGCACCAT ATTTGG

26

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGCTGCATG CCTCATGCTT CCCAGC

26

0001501.0349

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTTATTAA AGAGAGGGCT

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Leu	Pro	Ser	Ala	Ser	Arg	Glu	Arg	Pro	Gly	Tyr	Arg	Ala	Gly	Val	
1				5					10					15		
Ala	Ala	Pro	Asp	Leu	Leu	Asp	Pro	Lys	Ser	Ala	Ala	Gln	Asn	Ser	Lys	
			20					25					30			
Pro	Arg	Leu	Ser	Phe	Ser	Thr	Lys	Pro	Thr	Val	Leu	Ala	Ser	Arg	Val	
		35					40					45				
Glu	Ser	Asp	Thr	Thr	Ile	Asn	Val	Met	Lys	Trp	Lys	Thr	Val	Ser	Thr	
	50					55					60					
Ile	Phe	Leu	Val	Val	Val	Leu	Tyr	Leu	Ile	Ile	Gly	Ala	Thr	Val	Phe	
65					70					75					80	
Lys	Ala	Leu	Glu	Gln	Pro	His	Glu	Ile	Ser	Gln	Arg	Thr	Thr	Ile	Val	
				85					90					95		
Ile	Gln	Lys	Gln	Thr	Phe	Ile	Ser	Gln	His	Ser	Cys	Val	Asn	Ser	Thr	
		100						105					110			
Glu	Leu	Asp	Glu	Leu	Ile	Gln	Gln	Ile	Val	Ala	Ala	Ile	Asn	Ala	Gly	
		115					120					125				
Ile	Ile	Pro	Leu	Gly	Asn	Thr	Ser	Asn	Gln	Ile	Ser	His	Trp	Asp	Leu	
	130					135					140					
Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	Phe	
145					150					155					160	
Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	Ile	
				165				170						175		
Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	Gly	Val	
		180						185					190			
Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val	Glu	
		195					200					205				

00016011031197

0801601.031193

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
420 425

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CCATCCTAAT ACGACTCACT ATAGGGCTCG AGCGNCCGCC CGGGCAGTAA AATGCCTGCC	60
CGTGCAGCTC GGAGCGCGCA GCGCGTCTCT GAATAAGAAG TGAGTACAAT GCGTGTGTTG	120
TAAAAAAAAG CTTCAAGTCC GTCTTTTTC AAAAAACATTT TGAATGCTGC ATGCCTCATG	180
CTTCCCAGCG CCTCGCGGGA GAGACCCGGC TATAGAGCAG GAGTGGCGGC ACCTGACTTG	240
CTGGATCCTA AATCTGCCGC TCAGAACTCC AAACCGAGGC TCTCATTTTC CACGAAACCC	300
ACAGTGCTTG CTTCCCGGGT GGAGAGTGAC ACGACCATTA ATGTTATGAA ATGGAAGACG	360
GTCTCCACGA TATTCCTGGT GGTGTGCTC TATCTGATCA TCGGAGCCAC CGTGTTCAAA	420

GCATTGGAGC AGCCTCATGA GATTTCACAG AGGACCACCA TTGTGATCCA GAAGCAAACA	480
TTCATATCCC AACATTCCCTG TGTCAATTCG ACGGAGCTGG ATGAACTCAT TCAGCAAATA	540
GTGGCAGCAA TAAATGCAGG GATTATACCG TTAGGAAACA CCTCCAATCA AATCAGTCAC	600
TGGGATTTGG GAAGTTCCTT CTTCTTTGCT GGCACGTGTA TTACAACCAT AGGATTTGGA	660
AACATCTCAC CACGCACAGA AGGCGGCAAA ATATTCTGTA TCATCTATGC CTTACTGGGA	720
ATTCCCCTCT TTGGTTTTCT CTTGGCTGGA GTTGGAGATC AGCTAGGCAC CATATTTGGA	780
AAAGGAATTG CCAAAGTGGA AGATACGTTT ATTAAGTGGA ATGTTAGTCA GACCAAGATT	840
CGCATCATCT CAACAATCAT ATTTATACTA TTTGGCTGTG TACTCTTTGT GGCTCTGCCT	900
GCGATCATAT TCAAACACAT AGAAGGCTGG AGTGCCCTGG ACGCCATTTA TTTTGTGGTT	960
ATCACTCTAA CAACTATTGG ATTTGGTGAC TACGTTGCAG GTGGATCCGA TATTGAATAT	1020
CTGGACTTCT ATAAGCCTGT CGTGTGGTTC TGGATCCTTG TAGGGCTTGC TTACTTTGCT	1080
GCTGTCCTGA GCATGATTGG GAGATTGGTC CGAGTGATAT CTAAAAAGAC AAAAGAAGAG	1140
GTGGGAGAGT TCAGAGCACA CGCTGCTGAG TGGACAGCCA ACGTCACAGC CGAATTCAAA	1200
GAAACCAGGA GGCGACTGAG TGTGGAGATT TATGACAAGT TCCAGCGGGC CACCTCCATC	1260
AAGCGGAAGC TCTCGGCAGA ACTGGCTGGA AACCACAATC AGGAGCTGAC TCCTTGTAGG	1320
AGGACCCTGT CAGTGAACCA CCTGACCAGC GAGAGGGATG TCTTGCCCTCC CTTACTGAAG	1380
ACTGAGAGTA TCTATCTGAA TGGTTTGGCG CCACACTGTG CTGGTGAAGA GATTGCTGTG	1440
ATTGAGAACA TCAAATAGCC CTCTCTTTAA ATAACCTTAG GCATAGCCAT AGGTGAGGAC	1500
TTCTCTATGC TCTTTATGAC TGTTGCTGGT AGCATTTTTT AAATTGTGCA TGAGCTCAAA	1560
GGGGGAACAA AATAGATACA CCCATCATGG TCATCTATCA TCAAGAGAAT TTGGAATTCT	1620
GAGCCAGCAC TTTCTTTCTG ATGATGCTTG TTGAACGGCC CACTTTCTTT GATGAGTGGA	1680
ATGACAAGCA ATGTCTGATG CCTTTGTGTG CCCAGACTGT TTTCCCTCTCT CTTTCCCTAA	1740
TGTGCCATAA GGCCTCAGAA TGAATTGAGA ATTGTTTCTG GTAACAATGT AGCTTTGAGG	1800
GATCAGTTCT TAACTTTTCA GGGTCTACCT AACTGAGCCT AGATATGGAC CATTTATGGA	1860
TGACAACAAT TTTTTTTTTG TAAATGACAA GAAATTCCTA TGCAGCCTTT TACCTAAGAA	1920
ATTTCTGTCA GTGCCCTTATC TTATGAAGAA ACAGAACCTC TCTAGCTAAT GTGTGGTTTC	1980
TCCTTCCCTG CCCCCACCCC TAGGCTCACC TCTGCAGTCT TTTACCCAG TTCTCCCAT	2040
TGAATACCAT ACCTTGNTGG AAACAGNGTG TAAAATGACT GAAGTGATGA TGCCGAAGAT	2100
GAAATAGATG NCAAAATTAGN TGGACATTGA	2130

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAAAGATCTA AAATGCTTCC CAGCGCC

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGTCGACC TATTTGATGT TCTCAAT

27

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAAAAGCTTA AAATGCTTCC CAGCGCC

27

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAATCTAGAC TATTTGATGT TCTCAAT

27

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACAAAAACC TTTTTTGT TT TGAATGGCCT AGAGAGGGTA AGGGATCCCC TGACGAACAG

60

GAGCAGAGCC AGCTAGAACC TGGGCCTGGC CAGTTCAAGG CCACCAGAGG GCAGCCTTCT

120

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GCGGAAGGCA GTATTGGGGT AGGCAGGGAC CCCAGCAGAC ATGGCACTCA GAGCTCTCAC	180
TGTCCACTGA CTCTCTCTTC TCCAGGTTAT GGCCACATGG CCCCACTATC GCCAGGCGGA	240
AAGGCCTTCT GCATGGTCTT ATAGCCCTTG GGCTGCCAGC CTCCTTAGCT CTCGTGGCCA	300
CCCTGCGCCA TTGCCTGCTG CCTGTGCTCA GCCGCCACG TGCCTGGGTA GCGGTCCACT	360
GGCAGCTGTC ACCGGCCAGG GCTGCGCTGC TGCAGGCAGT TGCCTGGGA CTGCTGGTGG	420
CCAGCAGCTT TGTGCTGCTG CCAGCGCTGG TGCTGTGGGG CCTTCAGGGC GACTGCAGCC	480
TGCTGGGGGC CGTCTACTTC TGCTTCAGCT CGCTCAGCAC CATTGGCCTG GGG	533

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 956 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGATACGAT TTAATACGAC TCACTATAGG GAATTTGGCC CTCGAGGCCA AGAATTCGGC	60
ACGAGGAGAA TGTGCGCACG TTGGCTCTCA TCGTGTGCAC CTTACCTAC CTGCTGGTGG	120
GCGCCGCGGT GTTCGACGCA CTGGAGTCGG AGCCGGAGAT GATCGAGCGG CAGCGGCTGG	180
AGCTGCGGCA GCTGGAGCTG CGGGCGCGCT ACAACCTCAG CGAGGGCGGC TACGAGGAGC	240
TGGAGCGCGT CGTGCTGCGC CTCAAGCCGC ACAAGGCCGG CGTGCACTGG CGCTTCGCGG	300
GCTCCTTCTA CTTGCGCATC ACCGTCATCA CCACCATCGG CTATGGTCAT GCGGCGCCCA	360
GCACGGACGG AGGCAAGGTG TTCTGCATGT TCTACGCGCT GCTGGGCATC CCGCTCACAC	420
TAGTCATGTT CCAGAGCCTG GGTGAACGCA TCAACACCTC CGTGAGGTAC CTGCTGCACC	480
GTGCCAAGAG GGGGCTGGGC ATGCGGCACG CCGAAGTGTC CATGGCCAAC ATGGTGCTCA	540
TCGGTTTCGT GTCGTGCATC AGCACGCTGT GCATCGGCGC AGCTGCCTTC TCCTACTACG	600
AGCGCTGGAC TTTCTTCCAG GCCTATTACT ACTGCTTCAT CACCCTCACC ACCATCGGCT	660
TCGGCGACTA TGTGGCGCTG CAGAAGGACC AGGCGCTGCA GACGCAGCCG CAGTATGTGG	720
CTTCAGCTTC GTGTACATCC TCACGGGCTC ACGGTCATCG GCGCTTCCTC AACCTCGTGG	780
TGCTGCGATT CATGACCATG AACGCCGAGG ACGAGAAGCG TGATGCGGAG CACCGCGCCC	840
TGCTCACGCA CAACGGCCAG GCTGTCGGCC TGGGTGGCCT GAGCTGCCTG AGCGGTAGCC	900
TGGGCGACGG CGTGCGTCCC CGCGACCCAG TCACATGCGC TGCGGCCGCA AGCTTA	956

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTGAAACCAT GGGCCCGATA CCTGCTCCTG CTTATGGCCC ACCTGCTGGC CATGGGCCTT	60
GGGGCTGTGG TGCTTCAGGC CCTGGAGGGC CCTCCAGCTC GCCACCTCCA GGCCCAGGTC	120
CAGGCTGAAC TGGCTAGCTT CCAGGCAGAG CACAGGGCCT GCTTGCCACC TGAGGCCCTG	180
GAGGAGCTGC TAGGTGCGGT CCTGAGAGCA CAGGCCCATG GAGTTTCCAG CCTGGGCAAC	240
AGCTCAAGAC AAGCAACTGG GATCTGCCCT CAGCTCTGCT GTTCACTGCC AGCATCCTCA	300
CCACCACCGG TTATGGCCAC ATGGCCCCAC TCTCCTCAGG TGGAAAGGCC TTCTGTGTGG	360
TCTATGCAGC CCTTGGGCTG CCAGCCTCTC TAGCACTTGT GGCTGCCCTG CGCCACTGCT	420
TGCTGCCTGT GTTCAGTCGC CCAGGTGACT GGGTAGCCAT TCGCTGGCAG CTGGCACCAG	480
CTCAGGCTGC TCTGCTACAG GCAGCAGGAC TGGGCCTCCT GGTGGCCTGT GTCTTCATGC	540
TGCTGCCAGC ACTGGTGCTG TGGGGTGCTAC AGGGTGACTG GCAGCCTGCT AAACCATCTA	600
CTTCTGTTTC GGCTCACTCA GCACGATCGG CCTAGGAGAC TTGCTGCCTG CCCATGGACG	660
TGGCCTGCAC CCAGCCATTT ACCACCTTGG GCAGTTTGCA CTTCTTGGTT ACTTGCTCCT	720
GGGGCTCCTG GCCATGTTGT TAGCAGTAGA GACCTTCTCA GAGCTGCCTC AGGTCCGTGC	780
CATGGTGAAA TTCTTTGGGC CCAGTGGCTC TAGAACCGAT GAAGATCAAG ATGGCATCCT	840
AGGCCAAGAT GAGCTGGCTC TGAGCACTGT GCTGCCTGAC GCCCCAGTCT TGGGACCAAC	900
CACCCCAGCC TGAGCGGGAG GCACCAAGGA GTGCTTGAAG AACATAGCAG AAGGGTTATG	960
GGAATGAATA TGTCATGGGA TAATGTTAAT TTTAAAAATT AAATGGGCTG CTTAGCATGC	1020
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	1052

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser	
1 5 10 15	
Pro Asp Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe	
20 25 30	
Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly	
35 40 45	
Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr	
50 55 60	
Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly	
65 70 75 80	

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Gly 1	Ile	Trp	Pro	Ser 5	Arg	Pro	Arg	Ile	Arg 10	His	Glu	Glu	Asn	Val 15	Arg
Thr	Leu	Ala	Leu 20	Ile	Val	Cys	Thr	Phe 25	Thr	Tyr	Leu	Leu	Val 30	Gly	Ala
Ala	Val	Phe 35	Asp	Ala	Leu	Glu	Ser 40	Glu	Pro	Glu	Met	Ile 45	Glu	Arg	Gln
Arg	Leu 50	Glu	Leu	Arg	Gln	Leu 55	Glu	Leu	Arg	Ala	Arg 60	Tyr	Asn	Leu	Ser
Glu 65	Gly	Gly	Tyr	Glu	Glu 70	Leu	Glu	Arg	Val	Val 75	Leu	Arg	Leu	Lys	Pro 80
His	Lys	Ala	Gly	Val 85	Gln	Trp	Arg	Phe 90	Ala	Gly	Ser	Phe	Tyr	Phe 95	Ala
Ile	Thr	Val	Ile 100	Thr	Thr	Ile	Gly	Tyr 105	Gly	His	Ala	Ala	Pro 110	Ser	Thr
Asp	Gly	Gly 115	Lys	Val	Phe	Cys	Met 120	Phe	Cys	Met	Phe	Tyr 125	Ala	Leu	Leu
Gly	Ile 130	Pro	Leu	Thr	Leu	Val 135	Met	Phe	Gln	Ser	Leu 140	Gly	Glu	Arg	Ile
Asn 145	Thr	Ser	Val	Arg	Tyr 150	Leu	Leu	His	Arg	Ala 155	Lys	Arg	Gly	Leu	Gly 160
Met	Arg	His	Ala	Glu 165	Val	Ser	Met	Ala	Asn 170	Met	Val	Leu	Ile	Gly 175	Phe
Val	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala	Ala	Phe	Ser	Tyr

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180										185					190				
Tyr	Glu	Arg	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile	Thr				
		195					200					205							
Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu	Gln	Lys	Asp	Gln				
	210					215					220								
Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	Ser	Ala	Ser	Cys	Thr	Ser				
225					230					235					240				
Ser	Arg	Ala	His	Gly	His	Arg	Arg	Phe	Leu	Asn	Leu	Val	Val	Leu	Arg				
				245					250					255					
Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Asp	Ala	Glu	His	Arg				
			260					265					270						
Ala	Leu	Leu	Thr	His	Asn	Gly	Gln	Ala	Val	Gly	Leu	Gly	Gly	Leu	Ser				
	275						280					285							
Cys	Leu	Ser	Gly	Ser	Leu	Gly	Asp	Gly	Val	Arg	Pro	Arg	Asp	Pro	Val				
	290					295					300								
Thr	Cys	Ala	Ala	Ala	Ala	Ser	Leu												
305						310													

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Leu	Lys	Pro	Trp	Ala	Arg	Tyr	Leu	Leu	Leu	Leu	Met	Ala	His	Leu	Leu		
1				5					10					15			
Ala	Met	Gly	Leu	Gly	Ala	Val	Val	Leu	Gln	Ala	Leu	Glu	Gly	Pro	Pro		
		20						25					30				
Ala	Arg	His	Leu	Gln	Ala	Gln	Val	Gln	Ala	Glu	Leu	Ala	Ser	Phe	Gln		
		35					40					45					
Ala	Glu	His	Arg	Ala	Cys	Leu	Pro	Pro	Glu	Ala	Leu	Glu	Glu	Leu	Leu		
	50				55						60						
Gly	Ala	Val	Leu	Arg	Ala	Gln	Ala	His	Gly	Val	Ser	Ser	Leu	Gly	Asn		
65				70					75					80			
Ser	Ser	Xaa	Thr	Ser	Asn	Trp	Asp	Leu	Pro	Ser	Ala	Leu	Leu	Phe	Thr		
				85				90						95			
Ala	Ser	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser		
		100					105						110				
Ser	Gly	Gly	Lys	Ala	Phe	Cys	Val	Val	Tyr	Ala	Ala	Leu	Gly	Leu	Pro		
		115					120					125					
Ala	Ser	Leu	Ala	Leu	Val	Ala	Ala	Leu	Arg	His	Cys	Leu	Leu	Pro	Val		
	130					135					140						
Phe	Ser	Arg	Pro	Gly	Asp	Trp	Val	Ala	Ile	Arg	Trp	Gln	Leu	Ala	Pro		
145				150						155					160		

Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala
165 170 175

Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly
180 185 190

Asp Trp Gln Pro Ala Xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser
195 200 205

Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His
210 215 220

Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu
225 230 235 240

Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu
245 250 255

Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg
260 265 270

Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu
275 280 285

Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala
290 295 300

00015011 034497